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Impact of antiretroviral therapy on the biological profile of HIV infected children in Cameroon

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Background: HIV infection in children is a public health problem in ressource-constrained settings. Despite the support of the international community, meeting the cost of treatment and biological follow up remains a challenge in Cameroon and the developing world as a whole. The aim of this study was to evaluate the impact of antiretroviral therapy on the biological profile of HIV infected children followed up at the University Teaching Hospital of Yaounde (UTHY) in Cameroon.

Methods & Materials: We carried out a retrospective study from May 2003 to December 2012 at the paediatric service of the UTHY. 116 files of HIV infected children were studied. Data on the socio demographic characteristics, family history in relation to HIV, biological investigations and the treatment outcome were collected. We compared the results of biological investigations performed before and six months after the initiation of antiretroviral therapy. Data analysis was performed using EPI info and SPSS statistical software. The study was approved by the Cameroon ethics committee.

Results: The mean age was 54.02±46.34 months. The sex ratio was 0.96 in favor of males. This cohort was characterized by a late diagnosis (49.95±45 months) as well as a late initiation of antiretroviral therapy (8.52±14.17months). Patients consulted when the clinical and immunologic state was well advanced (74.2% and 83.3% respectively). Only 36 out of 116 children (31%) were able to meet the cost of biological investigations before and six months after the initiation of therapy. We noticed a significant increase in the following biological parameters after six months of therapy: blood glucose levels of 0.09 g/L (0.75-0.84; p= 0.007), percentage of CD4 in children below 5 years of age of 4.62% (20.12-24.75; p=0.022), absolute value of CD4 in children above 5 years of 294 cells/mm3 (151.18-445.18; p=0.011), CD4/CD8 ratio of 0.35 (0.55-0.90; p=0.000). Interestingly, after six months of therapy, there was a decrease in viral load of 3.90 log 10 copies/ml (5.85-1.95; p=0.006).

Conclusion: This study demonstrated that immune restoration and virologic suppression in children were obtained after six months of therapy. Therefore, making biological follow up affordable to this vulnerable group is essential in our quest for a good therapeutic outcome.

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Viruses in CSF of HIV patients with acute and late onset neurological conditions detected by NGS

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Background: Neurological symptoms are common in HIV-infected patients, with meningitis, stroke and seizures associated with acute onset conditions and neurocognitive disorders (HAND) common in late infection. Identifying a specific cause is difficult, with potential infectious aetiologies limited by the diagnostic repertoire available in the routine microbiology and virology laboratory. Next generation sequencing (NGS) is an unbiased approach to search for novel and other neurotropic infectious agents.

A NGS pilot study was undertaken to identify the viruses in cerebrospinal fluid (CSF) of HIV-infected patients presenting with a range of neurological symptoms.

Methods & Materials: Total nucleic acid was extracted from the CSF of 15 HIV-infected patients with meningitis (n=4), HAND (n=10) and young stroke (n=1). RNA was reverse transcribed and ss cDNA/DNA converted to ds DNA. The Nextera sample preparation kit was used for indexing and preparation of samples for sequencing on the Illumina MiSeq platform. Human and bacterial sequences were removed using DeconSeq and raw viral reads taxonomically characterized using the web-based METAVIR server.

Results: Neurotropic viruses, HIV and HHV6, were detected in 2/4 meningitis and 2/10 HAND cases. Other viruses identified were influenza virus A H1N1 (1 HAND case), flavivirus GBV-C (1 stroke and HAND case), TTV (1 stroke case) and human papillomavirus (1 HAND case). In 5 samples parvoviruses were detected. Bacteriophages from a range of bacterial hosts including Streptococcus, Pseudomonas, Enterobacteria, Lactobacillus and Staphylococcus, made up a significant proportion (up to 60%) of the viral sequences detected in all samples.

Conclusion: The paucity of neurotropic viral sequences detected in the CSF of this group of patients suggests that other factors were responsible for the neurological disease. The detection of influenza virus and GBV-C is surprising, but there is evidence that they may invade the CNS. Bacteriophages make up the vast majority of viruses found in the human virome from the gut and respiratory tract, but this is the first report of their ubiquitous presence in CSF. Sequencing using a different NGS platform may provide further evidence of viral infection in these patients.

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